

FIG. 1

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OP-1	CCA - - PTQLNAI SVLYFDDS- SNVI LKKYRNMVVRA	CGCH
BMP-5	CCA - - PTKLNAI SVLYFDDS- SNVI LKKYRNMVVRSC	CGCH
BMP-6	CCA - - PTKLNAI SVLYFDDN- SNVI LKKYRNMVVRA	CGCH
OP-2	CCA - - PTKLSATSVLYYDSS- NNVI LRKHRNMVVKAC	CGCH
OP-3	CCV - - PTELSAI SLLYYDRN- NNVI LRRERNMVVQAC	CGCH
60A	CCA - - PTRLGALPVL YHLND- ENVNLKKYRNMI VKSC	CGCH
Vg-1	CCV - - PTKMSPI SMLFYDNN- DNVVL RHYENMAVDEC	CGCR
UNIVIN	CCA - - PTKLSGI SMLYFDNN- ENVVL RQYEDMVVEAC	CGCR
BMP-2	CCV - - PTELSAI SMLYLDEN- EKVVL KNYQDMVVEGC	CGCR
BMP-4	CCV - - PTELSAI SMLYLDEY- DKVVL KNYQEMVVEGC	CGCR
GDF-5	CCV - - PTRLSPI SILFIDSA- NNVVYKQYEDMVVES	CGCR
GDF-6	CCV - - PTKLTPI SILYIDAG- NNVVYKQYEDMVVES	CGCR
GDF-7	CCV - - PARLSPI SILYIDAA- NNVVYKQYEDMVVEAC	CGCR
CDMP-2	CCV - - PTKLTPI SILYIDAG- NNVVYNEYEEMVVES	CGCR
dpp	CCV - - PTQLDSVAML YLNDQ- STVVL KNYQEMTVVGC	CGCR
BMP-9	CCV - - PTKLSPI SVLYKDDMGVPTL KYHYEGMSVAEC	CGCR
DORSALIN	CCV - - PTKLDAI SILYKDDAGVPTLI YNYEGMKVAEC	CGCR
BMP-10	CCV - - PTKLEPI SILYLDKG- VVTYKFKEYEGMAVSEC	CGCR
GDF-3	VCV - - PTKLSPI SMLYQDSD- KNVI LRHYEDMVVDEC	CGCG
GDF-1	CCV - - PERLSPI SVLFFDNE- DNVVL RHYEDMVVDEC	CGCR
SCREW	CCV - - PTVLGAI TILRYLNE- DIIDLTKYQKAVAKE	CGCH
BMP-3	CCV - - PEKMSSL SILFFDEN- KNVVLKVYPNMTVES	CACR
NODAL	CCA - - PVKTKPLSMLYVDN- - GRVLL EHHKDMI VEE	CGCL
TGF- α 2	CCV - - SQDLEPLTILYYIG- - KTPKIEQLSNMI VKSC	CKCS
TGF- α 3	CCV - - PQDLEPLTILYYVG- - RTPKVEQLSNMVVKSC	CKCS
TGF- α 4	CCV - - PQTLDPLPIIYYVG- - RNV RVEQLSNMVVRAC	CKCS
TGF- α 1	CCV - - PQALEPLPIVYYVG- - RKP KVEQLSNMI VRSC	CKCS
TGF- α 5	CCV - - PDVLEPLPIIYYVG- - RTAKVEQLSNMVVRSC	CNCS
GDF-9	SCV - - PGKYSPLSVLTI EPD- GSI AYKEYEDMI ATRCT	CR
Inhibin α	CCAALPGTMRPLHVRTTSDGGYSFKYETVPNLLTQHCA	CI
Inhibin β A	CCV - - PTKLRPM SMLYYDDG- QNI I KKDI QNMI VEE	CGCS
Inhibin β B	CCI - - PTKLSTMSMLYFDDE- YNI VKRDVPNMI VEE	CGCA
Inhibin β C	CCV - - PTARRPLSLLYYDRD- SNI VKTDI PDMVVEAC	CGCS
MIS	CCV - - PTATAGKLLI SLSE- - ERI SAHHVPNMVATE	CGCR
GDNF	CCR - - PIAFDDD- - LSFLD- - DNLVYHI LRKHS AKRC	CGCI
BMP-11	CCT - - PTKMSPINMLYFNDK- QQI I YGKI PGMVVDR	CGCS
GDF-9	SCV - - PGKYSPLSVLTI EPD- GSI AYKEYEDMI ATRCT	CR

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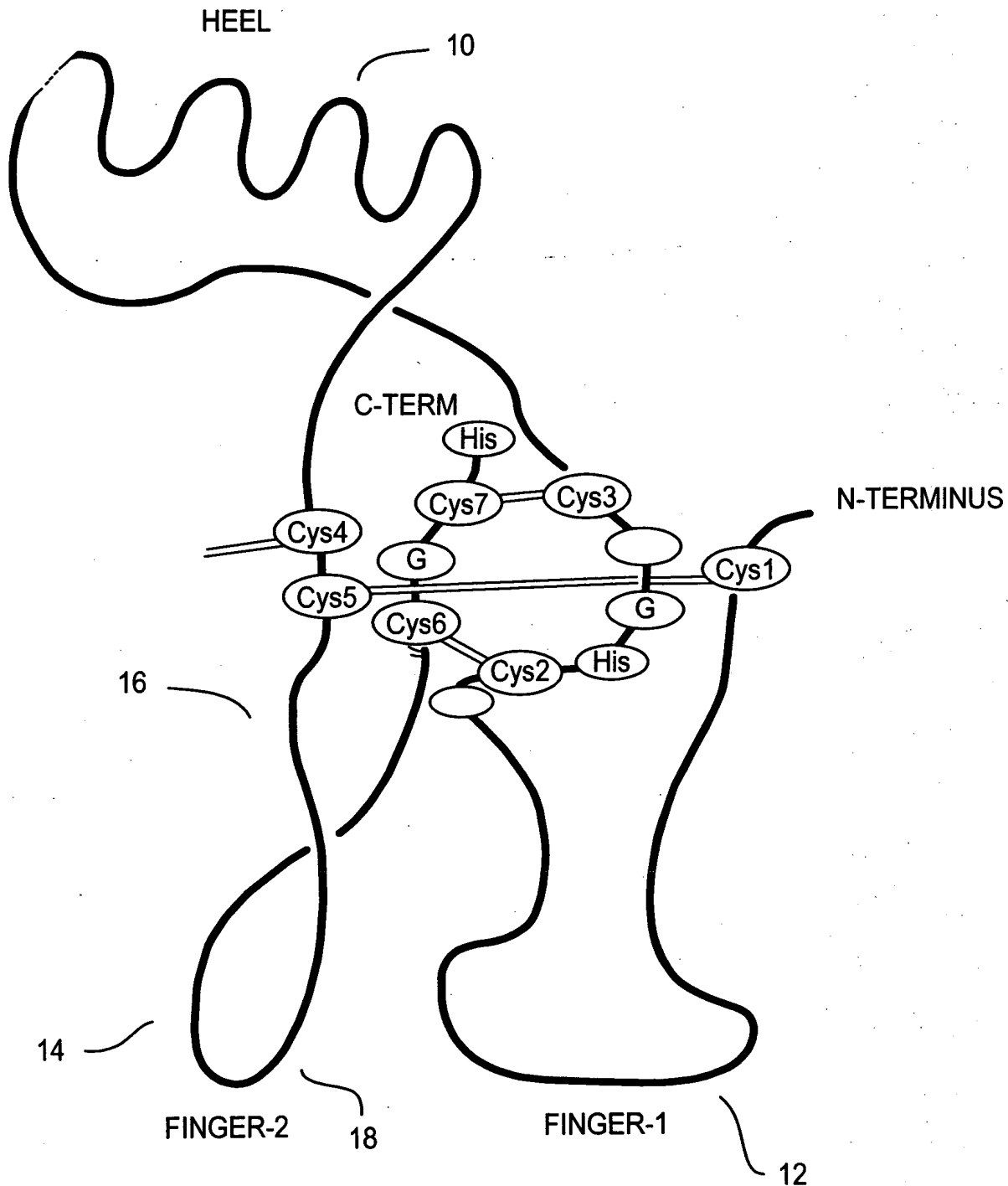


FIG.2

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7-CYSTEINE DOMAIN OF OP-1

FINGER-1

TGTAAGAAGCAGAGCTGTATGTCAGCTCCGAGACCTGGGCTGGCAGGACTGGATCATCGCGCTGAAGGCTACGCCGCCTACTACTGTGAGGGG
C K K H E L Y V S F R D L G W Q D W I I A P E G Y A A Y Y C E G

HEEL

GAGTGTGCCTTCCCTCTGAACCTCTACATGAACGCCACCAACCCAGCCATCGTGCAGACGCTGGTCCACTTCATCAACCCGGAAACGGTGCCCAAGCCCTGC
E C A F P L N S Y M N A T N H A I V Q T L V H F I N P E T V P K P C

FINGER-2

TGTGCGCCCGCAGCTCAATGCCATCTCCGTCTCTACTTCGATGACAGCTCCAACGTCATCCTGAAGAAATACAGAAACATGGTGGTCCGGGCGCTGTGGCTGCCAC
C A P T Q L N A I S V L Y F D D S S N V I L K K Y R N M V V R A C G C H

FIG. 3

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OP-1 CHIMERICS WITH CDMP-2 OR WITH BMP-2

PARENTAL MOLECULES:

REFOLDING ACTIVITY (CELL BASED)

	FINGER1	HEEL	FINGER2			
OP-1				h	(-)	+++ (*)
BMP-2				r	+++	+++
CDMP-2				r	++++	+/-

REPLACING FINGER-1 OR HEEL:

H2383				r	+/-	N/A
H2362				r	+	N/A
H2360				r	+	N/A
H2331				r	+	N/A

REPLACING FINGER-2 OR HEEL:

H2389				r	+++	+++
H2471				r	+++	+++
H2388				r	+++	+/-
H2410				r	+++	+++
H2429				r	+/-	N/A

CHANGING PATCHES OF RESIDUES:

H2381				r	+++	N/A
H2390				r	+	N/A
H2396				r	+	N/A
H2421				r	+/-	N/A



PAIRED CHANGES IN FINGER-2:

H2418				r	+++	++
H2420				r	++++	+/-

FIG. 4A

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OP-1 MUTANTS WITH C-TERMINAL ARGININE INSTEAD OF HISTIDINE:

H2247		+	+++
H2233		+	+++

BALANCING OF CHARGED RESIDUES IN FINGER-2 OF OP-1 MUTANTS:






H2406		+/-	N/A
H2443		+++	++
H2447		+++	++
H2433		+/-	N/A
H2456		+++	+++

FIG. 4B

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**CORRELATION OF REFOLDING EFFICIENCY AND CHARGED AMINO ACIDS
IN THE TGF- β (SEVEN CYSTEINE) DOMAIN**

PROTEIN	FINGER-1	CXGXC	HEEL	FINGER-2	CXCX C-TERM	TOTAL OF CHARGED RESIDUES (+), (-) = TOTAL	NEGATIVE CHARGES, FINGER-2	NET CHARGES, FINGER-2	REFOLDING EFFICIENCY
OP-1	3+, 4-	2-	1+, 1-	4+, 2-	0	8+, 9- = 17	2-	2+	+/-
H2247	3+, 4-	2-	1+, 1-	4+, 2-	1+	9+, 9- = 18	2-	2+	+
H2447	3+, 4-	2-	1+, 1-	2+, 6-	1+	7+, 12- = 19	6-	4-	+++
BMP-3	4+, 4-	0	3+, 1-	3+, 4-	1+	11+, 9- = 20	4-	1-	+++
BMP-2	2+, 3-	1-	2+, 1-	2+, 6-	1+	7+, 11- = 18	6-	4-	+++
GDF-5	3+, 5-	1-	1+, 4-	2+, 4-	1+	6+, 14- = 20	4-	2-	+++
CDMP-2	3+, 5-	1-	1+, 3-	2+, 4-	1+	6+, 13- = 19	4-	2-	+++
GDNF	2+, 4-	0	6+, 4-	5+, 5-	0	13+, 13- = 26	5-	0	+++
TGF- β 1	5+, 3-	0	1+, 1-	5+, 2-	1+	11+, 6- = 17	2-	3+	+/-
TGF- β 2	5+, 3-	0	1+, 2-	4+, 3-	1+	10+, 8- = 18	3-	1+	+/-

FIG. 5

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TGF- β SUBGROUP																																			
TGF- β 1:	C	C	V	R	Q	L	Y	I	D	F	R	K	D	L	G	W	K	-	W	I	H	E	P	K	G	Y	H	A	N	F	C	L	G	P	C
TGF- β 2:	C	C	L	R	P	L	Y	I	D	F	K	R	D	L	G	W	K	-	W	I	H	E	P	K	G	Y	N	A	N	F	C	A	G	A	C
TGF- β 3:	C	C	V	R	P	L	Y	I	D	F	R	Q	D	L	G	W	K	-	W	V	H	E	P	K	G	Y	Y	A	N	F	C	S	G	P	C
TGF- β 4:	C	C	V	R	P	L	Y	I	D	F	R	K	D	L	Q	W	K	-	W	I	H	E	P	K	G	Y	M	A	N	F	C	M	G	P	C
TGF- β 5:	C	C	V	K	P	L	Y	I	N	F	R	K	D	L	G	W	K	-	W	I	H	E	P	K	G	Y	E	A	N	Y	C	L	G	N	C
PATTERN:	C	C	V	R	P	L	Y	I	D	F	R	n	D	L	G	W	K	-	W	I	H	E	P	K	G	Y	X	A	N	F	C	X	G	j	C
Vg/dpp SUBGROUP																																			
dpp:	C	R	R	H	S	L	Y	V	D	F	S	-	D	V	G	W	D	D	W	I	V	A	P	L	G	Y	D	A	Y	Y	C	H	G	K	C
Vg-1:	C	K	K	R	H	L	Y	V	E	F	K	-	D	V	G	W	Q	N	W	V	I	A	P	Q	G	Y	M	A	N	Y	C	Y	G	E	C
Vgr-1:	C	K	K	H	E	L	Y	V	S	F	Q	-	D	L	G	W	Q	D	W	I	I	A	P	K	G	Y	A	A	N	Y	C	D	G	E	C
60A:	C	Q	M	Q	T	L	Y	I	D	F	K	-	D	L	G	W	H	D	W	I	I	A	P	E	G	Y	G	A	F	Y	C	S	G	E	C
BMP-2A:	C	K	R	H	P	L	Y	V	D	F	S	-	D	V	G	W	N	D	W	I	V	A	P	P	G	Y	H	A	F	Y	C	H	G	E	C
DORSALIN:	C	R	R	T	S	L	H	V	N	F	K	-	E	I	G	W	D	S	W	I	I	A	P	K	D	Y	E	A	F	E	C	K	G	G	C
BMP-2B/BMP-4:	C	R	R	H	S	L	Y	V	D	F	S	-	D	V	G	W	N	D	W	I	V	A	P	P	G	Y	Q	A	F	Y	C	H	G	D	C
BMP-3:	C	A	R	R	Y	L	Y	V	D	F	A	-	D	I	G	W	S	E	W	I	I	S	P	K	S	F	D	A	Y	Y	C	S	G	A	C
BMP-5:	C	K	K	H	E	L	K	V	S	F	R	-	D	L	G	W	Q	D	W	I	I	A	P	E	G	Y	A	A	F	Y	C	D	G	E	C
BMP-6:	C	R	K	H	E	L	Y	V	S	F	Q	-	D	L	G	W	Q	D	W	I	I	A	P	K	G	Y	A	A	N	Y	C	D	G	E	C
OP-1/BMP-7:	C	K	K	H	E	L	Y	V	S	F	R	-	D	L	G	W	Q	D	W	I	I	A	P	E	G	Y	A	A	Y	Y	C	E	G	E	C
OP-2:	C	R	R	H	E	L	Y	V	S	F	Q	-	D	L	G	W	L	D	W	V	I	A	P	Q	G	Y	S	A	Y	Y	C	E	G	E	C
OP-3:	C	R	R	H	E	L	Y	V	S	F	R	-	D	L	G	W	L	D	S	V	I	A	P	Q	G	Y	S	A	Y	Y	C	A	G	E	C
PATTERN:	C	n	n	r	r	L	Y	V	r	F	r	-	D	c	G	W	r	D	W	I	I	A	P	p	G	Y	X	A	d	Y	C	r	G	k	C
GDF SUBGROUP																																			
GDF-1:	C	R	T	R	R	L	H	V	S	F	R	-	E	V	G	W	H	R	W	V	I	A	P	R	G	F	L	A	N	F	C	Q	G	T	C
GDF-3:	C	H	R	H	Q	L	F	I	N	F	Q	-	D	L	G	W	H	K	W	V	I	A	P	K	G	F	M	A	N	Y	C	H	G	E	C
GDF-9:	C	E	L	H	D	F	R	L	S	F	S	-	Q	L	K	W	D	N	W	I	V	A	P	H	R	Y	N	P	R	Y	C	K	G	D	C
PATTERN:	C	r	X	r	r	f	X	c	r	F	r	-	r	c	X	W	r	r	W	a	a	A	P	r	X	d	X	j	r	d	C	r	G	r	C
INHIBIN SUBGROUP																																			
INHIBIN α :	C	H	R	V	A	L	N	I	S	F	Q	-	E	L	G	W	E	R	W	I	V	Y	P	P	S	F	I	F	H	Y	C	H	G	G	C
INHIBIN β A:	C	C	K	K	Q	F	F	V	S	F	K	-	D	I	G	W	N	D	W	I	I	A	P	S	G	Y	H	A	N	Y	C	E	G	E	C
INHIBIN β B:	C	C	R	Q	Q	F	F	I	D	F	R	-	L	I	G	W	N	D	W	I	I	A	P	T	G	Y	Y	G	N	Y	C	E	G	S	C
PATTERN:	C	X	n	X	X	f	X	a	r	F	P	-	X	c	G	W	m	r	W	I	a	X	P	j	j	d	X	X	r	Y	C	r	G	X	C
	1	BETA				10	HELIX				20	LOOP				30	BETA				RING														
	K									FINGER 1												KNOT A													

FIG. 6A

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TGF- β SUBGROUP																																											
TGF- β 1:	P	Y	I	W	S	-	-	-	-	-	-	L	D	T	Q	Y	S	K	V	L	A	L	Y	N	Q	H	N		P	-	-	G	A	S	A	A	P		C		C		
TGF- β 2:	P	Y	L	W	S	-	-	-	-	-	-	S	D	T	Q	H	S	R	V	L	S	L	Y	N	T	I	N		P	-	-	E	A	S	A	S	P		C		C		
TGF- β 3:	P	Y	L	R	S	-	-	-	-	-	-	A	D	T	T	H	S	T	V	L	G	L	Y	N	T	L	N		P	-	-	E	A	S	A	S	P		C		C		
TGF- β 4:	P	Y	I	W	S	-	-	-	-	-	-	A	D	T	Q	Y	T	K	V	L	A	L	Y	N	Q	H	N		P	-	-	G	A	S	A	A	P		C		C		
TGF- β 5:	P	Y	I	W	S	-	-	-	-	-	-	M	D	T	Q	Y	S	K	V	L	S	L	Y	N	Q	N	N		P	-	-	G	A	S	I	S	P		C		C		
PATTERN:	P	Y	c	W	S	-	-	-	-	-	-	X	D	T	Q	e	S	n	V	L	j	L	Y	N	r	X	N		P	-	-	X	A	S	A	j	P		C		C		
Vg/dpp SUBGROUP																																											
dpp:	P	F	P	L	A	D	H	F	-	-	-	N	S	T	N	H	A	V	V	Q	T	L	V	N	N	M	N		P	-	-	G	K	V	P	K	A		C		C		
Vg-1:	P	Y	P	L	T	E	I	L	-	-	-	N	G	S	N	H	A	I	L	Q	T	L	V	H	S	I	E		P	-	-	E	D	I	P	L	P		C		C		
Vgr-1:	S	F	P	L	N	A	H	M	-	-	-	N	A	T	N	H	A	I	V	Q	T	L	V	H	L	M	N		P	-	-	E	Y	V	P	K	P		C		C		
60A:	N	F	P	L	N	A	H	M	-	-	-	N	A	T	N	H	A	I	V	Q	T	L	V	H	L	L	E		P	-	-	K	K	V	P	K	P		C		C		
BMP-2A:	P	F	P	L	A	D	H	L	-	-	-	N	S	T	N	H	A	I	V	Q	T	L	V	N	S	V	N		-	-	-	S	K	I	P	K	A		C		C		
DORSALIN:	F	F	P	L	T	D	N	V	-	-	-	T	P	T	K	H	A	I	V	Q	T	L	V	H	L	Q	N		P	-	-	K	K	A	S	K	A		C		C		
BMP-2B/BMP-4:	P	F	P	L	A	D	H	L	-	-	-	N	S	T	N	H	A	I	V	Q	T	L	V	N	S	V	N		-	-	-	S	S	I	P	K	A		C		C		
BMP-3:	Q	F	P	M	P	K	S	L	-	-	-	K	P	S	N	H	A	T	I	Q	S	L	V	R	A	V	G		V	-	-	P	G	I	P	E	P		C		C		
BMP-5:	S	F	P	L	N	A	H	M	-	-	-	N	A	T	N	H	A	I	V	Q	T	L	V	H	L	M	F		P	-	-	D	H	V	P	K	P		C		C		
BMP-6:	S	F	P	L	N	A	H	M	-	-	-	N	A	T	N	H	A	I	V	Q	T	L	V	H	L	M	N		P	-	-	E	Y	V	P	K	P		C		C		
OP-1/BMP-7:	A	F	P	L	N	S	Y	M	-	-	-	N	A	T	N	H	A	I	V	Q	T	L	V	H	F	I	N		P	-	-	E	T	V	P	K	P		C		C		
OP-2:	S	F	P	L	D	S	C	M	-	-	-	N	A	T	N	H	A	I	L	Q	S	L	V	H	L	M	K		P	-	-	N	A	V	P	K	A		C		C		
OP-3:	I	Y	P	L	N	S	C	M	-	-	-	N	S	T	N	H	A	T	M	Q	A	L	V	H	L	M	K		P	-	-	D	I	I	P	K	V		C		C		
PATTERN:	X	F	P	L	X	X	X	b	-	-	-	N	j	T	N	H	A	I	a	Q	T	L	V	r	X	c	r		z	z	-	r	X	a	P	K	j		C		C		
GDF SUBGROUP																																											
GDF-1:	A	L	P	E	T	L	R	G	P	G	G	P	P	A	L	N	H	A	V	L	R	A	L	M	H	A	A	A		P	T	-	P	G	A	G	S	P		C		C	
GDF-3:	P	F	S	M	T	T	Y	L	-	-	-	N	S	S	N	Y	A	F	M	Q	A	L	M	H	M	A	D		-	-	-	P	K	V	P	K	A		V		C		
GDF-9:	P	R	A	V	R	H	R	Y	-	-	-	G	S	P	V	H	T	M	V	Q	N	I	I	Y	E	K	L		D	-	-	P	S	V	P	R	P		S		C		
PATTERN:	j	X	j	X	r	X	X	X	z	z	z	X	j	X	X	e	j	f	c	p	X	c	c	e	X	X	X		z	z	-	P	X	X	j	r	j		X		C		
INHIBIN SUBGROUP																																											
INHIBIN α :	G	L	H	I	P	P	N	L	S	L	-	-	P	V	P	G	A	P	P	T	P	A	Q	P	Y	S	L	-	-	-	-	L	P	G	A	Q	P		C		C		
INHIBIN β A:	P	S	H	I	A	G	T	S	G	S	-	-	S	L	S	F	H	S	T	V	I	N	H	Y	R	M	R	G		H	S	P	F	A	N	L	K	S		C		C	
INHIBIN β B:	P	A	Y	L	A	G	V	P	G	S	-	-	A	S	S	F	H	T	A	V	V	N	Q	Y	R	M	R	G		L	N	-	P	G	T	V	N	S		C		C	
PATTERN:	j	X	e	c	j	j	X	X	j	X	-	-	j	X	j	X	X	j	j	X	X	X	r	X	X	X	X	z		z	z	z	X	j	X	X	r	j		C		C	

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TGF- β SUBGROUP																																						
TGF- β 1:	V	-	P	Q	A	L	E	P	L	P	I	V	Y	Y	V	G	-	R	K	P	K	V	E	Q	L	S	N	M	I	V	R	S	C	K	C	S		
TGF- β 2:	V	-	S	Q	D	L	E	P	L	T	I	L	Y	Y	I	G	-	K	T	P	K	I	E	Q	L	S	N	M	I	V	K	S	C	K	C	S		
TGF- β 3:	V	-	P	Q	D	L	E	P	L	T	I	L	Y	Y	V	G	-	R	T	P	K	V	E	Q	L	S	N	M	V	V	K	S	C	K	C	S		
TGF- β 4:	V	-	P	Q	T	L	D	P	L	P	I	I	Y	Y	V	G	-	R	N	V	R	V	E	Q	L	S	N	M	V	V	R	A	C	K	C	S		
TGF- β 5:	V	-	P	D	V	L	E	P	L	P	I	I	Y	Y	V	G	-	R	T	A	K	V	E	Q	L	S	N	M	V	V	R	S	C	N	C	S		
PATTERN:	V	-	P	Q	X	L	E	P	L	j	I	c	Y	Y	V	G	-	R	r	j	K	V	E	Q	L	S	N	M	a	V	n	S	C	K	C	S		
Vg/dpp SUBGROUP																																						
dpp:	V	-	P	T	Q	L	D	S	V	A	M	L	Y	L	N	D	Q	-	S	T	V	V	L	K	N	Y	Q	E	M	T	V	V	G	C	G	C	R	
Vg-1:	V	-	P	T	K	M	S	P	I	S	M	L	F	Y	D	N	N	-	D	N	V	V	L	R	H	Y	E	N	M	A	V	D	E	C	G	C	R	
Vgr-1:	A	-	P	T	K	L	N	A	I	S	V	L	Y	F	D	D	N	-	S	N	V	I	L	K	K	Y	R	N	M	V	V	R	A	C	G	C	H	
60A:	A	-	P	T	R	L	G	A	L	P	V	L	Y	H	L	N	D	-	E	N	V	N	L	K	K	Y	R	N	M	I	V	K	S	C	G	C	H	
BMP-2A:	V	-	P	T	E	L	S	A	I	S	M	L	Y	L	D	E	N	-	E	K	V	V	L	K	N	Y	Q	D	M	V	V	E	G	C	G	C	R	
DORSALIN:	V	-	P	T	K	L	D	A	I	S	I	L	Y	K	D	D	A	G	V	P	T	L	I	Y	N	Y	E	G	M	K	V	A	E	C	G	C	R	
BMP-2B/BMP-4:	V	-	P	T	E	L	S	A	I	S	M	L	Y	L	D	E	Y	-	D	K	V	V	L	K	N	Y	Q	E	M	V	V	E	G	C	G	C	R	
BMP-3:	V	-	P	E	K	M	S	S	L	S	I	L	F	F	D	E	N	-	K	N	V	V	L	K	V	Y	P	N	M	T	V	E	S	C	A	C	R	
BMP-5:	A	-	P	T	K	L	N	A	I	S	V	L	Y	F	D	D	S	-	S	N	V	I	L	K	K	Y	R	N	M	V	V	R	S	C	G	C	H	
BMP-6:	A	-	P	T	K	L	N	A	I	S	V	L	Y	F	D	D	N	-	S	N	V	I	L	K	K	Y	R	N	M	V	V	R	A	C	G	C	H	
OP-1/BMP-7:	A	-	P	T	Q	L	N	A	I	S	V	L	Y	F	D	D	S	-	S	N	V	I	L	K	K	Y	R	N	M	V	V	R	A	C	G	C	H	
OP-2:	A	-	P	T	K	L	S	A	T	S	V	L	Y	Y	D	S	S	-	N	N	V	I	L	R	K	H	R	N	M	V	V	K	A	C	G	C	H	
OP-3:	V	-	P	T	E	L	S	A	I	S	L	L	Y	Y	D	R	N	-	N	N	V	I	L	R	R	E	R	N	M	V	V	Q	A	C	G	C	H	
PATTERN:	X	-	P	T	_p	L	_r	A	_a	S	_c	L	_Y	f	D	_m	_r	z	r	r	V	_a	L	_n	r	Y	p	i	M	X	V	p	j	C	G	C	r	
GDF SUBGROUP																																						
GDF-1:	V	-	P	E	R	L	S	P	I	S	V	L	F	F	D	N	S	-	D	N	V	V	L	R	H	Y	E	D	M	V	V	D	E	C	G	C	R	
GDF-3:	V	-	P	T	K	L	S	P	I	S	M	L	Y	Q	D	S	D	-	K	N	V	I	L	R	H	Y	E	D	M	V	V	D	E	C	G	C	R	
GDF-9:	V	-	P	G	K	Y	S	P	L	S	V	L	T	I	E	P	D	-	G	S	I	A	Y	K	E	Y	E	D	M	I	A	T	R	C	T	C	R	
PATTERN:	V	-	P	X	_n	f	S	P	_c	S	_c	L	X	X	k	X	r	-	X	r	a	X	f	_n	r	Y	E	D	M	a	X	r	p	j	C	X		
INHIBIN SUBGROUP																																						
INHIBIN α :	A	A	L	P	G	T	M	R	P	L	H	V	R	T	T	S	D	G	G	Y	S	F	K	Y	E	T	V	P	N	L	L	T	Q	H	C	A	C	I
INHIBIN β A:	V	-	P	T	K	L	R	P	M	S	M	L	Y	Y	D	D	G	-	Q	N	I	I	K	K	D	I	Q	N	M	I	V	E	E	C	G	C	S	
INHIBIN β B:	I	-	P	T	K	L	S	T	M	S	M	L	Y	F	D	D	E	-	Y	N	I	V	K	R	D	V	P	N	M	I	V	E	E	C	G	C	A	
PATTERN:	X	z	z	P	j	r	b	r	j	b	r	c	X	X	X	r	D	X	z	X	r	f	X	X	p	r	a	X	N	b	c	X	o	r	C	h	C	X
										80						90						100						110										
										BETA					LOOP					BETA					RING													
															FINGER 2										KNOT2C													

FIG. 6C

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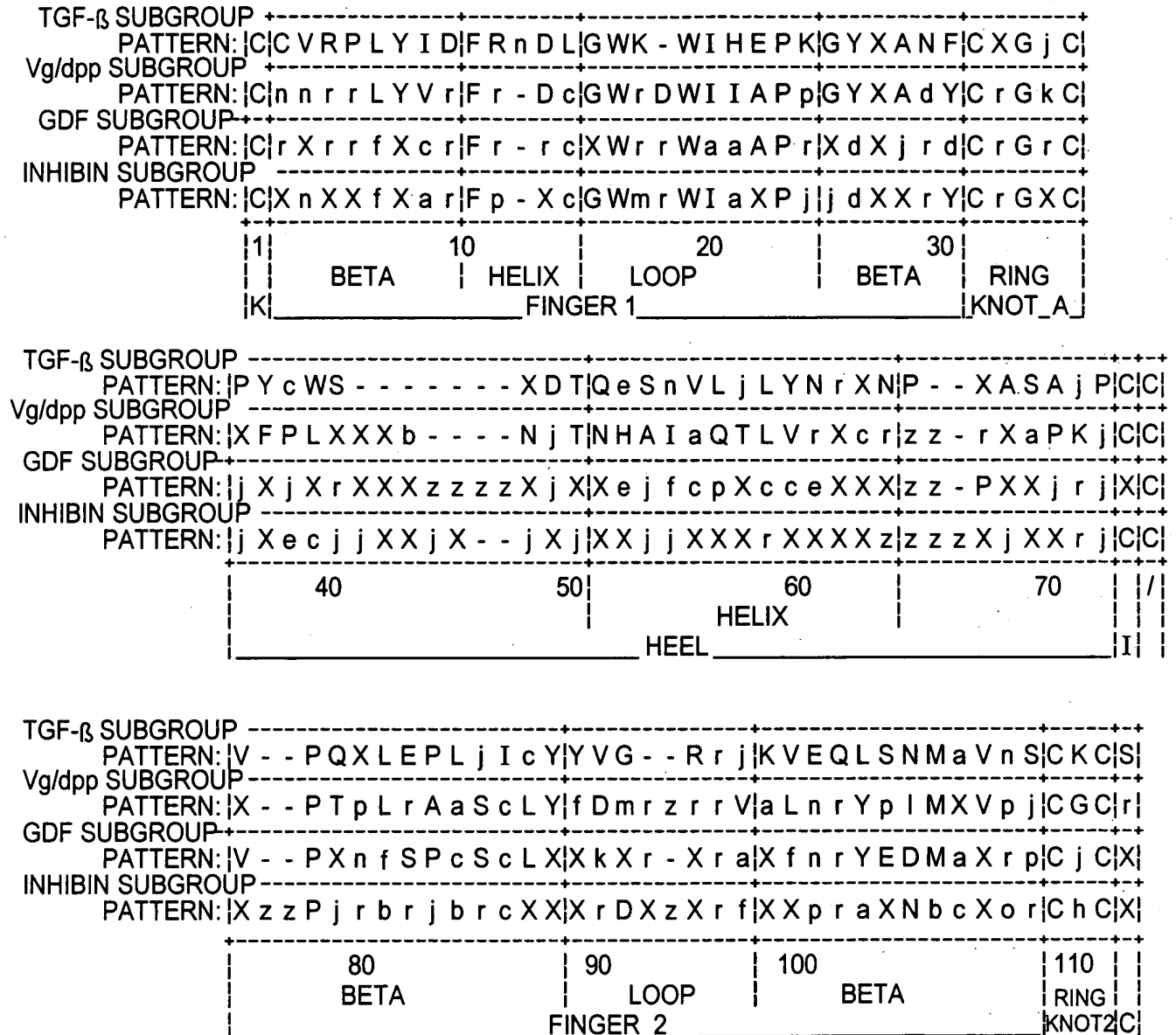


FIG. 7

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